Hereditas 71: 289—300 (1972)

Partitioning of an allopolyploid

K. A. SIDDIQUI

Atomic Energy Agricultural Research Centre, Tandojam, West Pakistan
Department of Agricultural Research, Danish Atomic Energy Commission
Research Establishment Risö, Roskilde, Denmark

(Received March 6, 1972)

Partitioning of the constituent genomes and chromosomes offers unique opportunities of analysing the genetic diploidization of the allohexaploid, *Triticum aestivum* (2n = 6x = 42 = = AABBDD). An extension of the existing aneuploid analysis is necessary to study the positive effects of individual chromosomes on a uniformly homozygous genetic background. Partitioning of *Triticum aestivum* can be initiated by extracting the three possible tetraploid ancestral components. Extraction of ancestral components may be accomplished either by producing pentaploids involving natural or synthetic tetraploids followed by a series of backcrosses to reconstitute *aestivum* genotype (backcross extraction method) or by producing multiple monosomics (monosomic method). The accuracy of depolyploidization can be tested by comparing the reconstituted tetraploids extracted by the two methods. A monosomic method of extraction is outlined and discussed. Backcross extraction itself can be a potential source of aneuploids. A new method for producing monosomics is proposed. These monosomics would serve to substantiate the results of extraction studies and partition analysis. Use of synthetic tetraploids restricts the success of backcross extraction owing to the sterility and genetic necrosis in pentaploids. Synthetic allopolyploids, however, have special advantages in extraction studies. Schemes for studying ancestral diploid components of natural allotetraploids and allohexaploids are proposed. Partitioning of allopolyploids presents the possibilities of reconstruction of their entire cytogenetic structure and of the synthesis of new species. The theoretical and practical implications of partitioning are discussed with reference to its utilization in studying the changes which the diploids and polyploids have undergone during evolution.

1. Analytical problems of an allopolyploid

The genetic and cytological versatility of allopolyploids presents many problems which require analysis and offers many opportunities of exploitation of mutations, recombinations and interactions. This paper is an extension of some ideas presented earlier (SIDDIQUI 1963, 1964, 1969a) and is concerned with some proposals aimed at the resolution of some analytical problems of an allopolyploid, *Triticum aestivum* (L.) THELL (2n = 6x = 42), the bread wheat, in which the three genomes A, B, and D have functioned together for some thousands of generations during evolution. Conventional genetic studies made during the last 70 years (BIFFEN 1905; HOWARD and HOWARD 1912; PERCIVAL 1921; MATSUURA 1933; VAVILOV 1951; AUSEMUS 1956; AUSEMUS et al. 1967; KUCKUCK 1970) have on the whole been unrewarding because relatively few major genes have been found in wheat, and the presence of many triplicated factors (SEARS 1969) has further complicated the analysis (SIDDIQUI 1969a).

The most significant contribution to the cytogenetics of *Triticum aestivum* has been the development of monosomic (2n = 41) and nullisomic (2n = 40) series by SEARS (1939, 1944, 1954). This development has made it possible to associate some visible morphological effects with the absence of a chromosome or a pair of chromosomes. Monosomics and nullisomics have